

cgctctagcc cggtgggaag ctttcatcca gaaca atg aat ttc ata aag gac	53
Met Asn Phe Ile Lys Asp	
1 5	
aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa	101
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln	
10 15 20	
atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta	149
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val	
25 30 35	
aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc	197
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile	
40 45 50	
att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt	245
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu	
55 60 65 70	
aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga	293
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly	
75 80 85	
caa agt ctt ttt cat cag aca tca gaa gga gac ttg gac gat ttg gct	341
Gln Ser Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp Asp Leu Ala	
90 95 100	
cag gat tta aag gac ttg tac cat acc cca tct ttt ctg aac ttt tat	389
Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu Asn Phe Tyr	
105 110 115	
ccc ctt ggt gaa gat att gac att att ttt aac ttg aaa agc acc ttc	437
Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe Asn Leu Lys Ser Thr Phe	
120 125 130	
aca gaa cct gtc ctg tgg agg aag gac caa cac cat cac cgc gtg gag	485
Thr Glu Pro Val Leu Trp Arg Lys Asp Gln His His His Arg Val Glu	
135 140 145 150	
cag ctg acc ctg aat ggc ctc ctg cag gct ctt cag agc ccc tgc atc	533
Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala Leu Gln Ser Pro Cys Ile	
155 160 165	
att gaa ggg gaa tct ggc aaa ggc aag tcc act ctg ctg cag cgc att	581
Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser Thr Leu Leu Gln Arg Ile	
170 175 180	
gcc atg ctc tgg ggc tcc gga aag tgc aag gct ctg acc aag ttc aaa	629
Ala Met Leu Trp Gly Ser Gly Lys Cys Lys Ala Leu Thr Lys Phe Lys	
185 190 195	
ttc gtc ttc ttc ctc cgt ctc agc agg gcc cag ggt gga ctt ttt gaa	677
Phe Val Phe Phe Leu Arg Leu Ser Arg Ala Gln Gly Gly Leu Phe Glu	
200 205 210	

Fig. 1A

acc ctc tgt gat caa ctc ctg gat ata cct ggc aca atc agg aag cag	725
Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro Gly Thr Ile Arg Lys Gln	
215 220 225 230	
aca ttc atg gcc atg ctg ctg aag ctg cgg cag agg gtt ctt ttc ctt	773
Thr Phe Met Ala Met Leu Leu Lys Leu Arg Gln Arg Val Leu Phe Leu	
235 240 245	
ctt gat ggc tac aat gaa ttc aag ccc cag aac tgc cca gaa atc gaa	821
Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln Asn Cys Pro Glu Ile Glu	
250 255 260	
gcc ctg ata aag gaa aac cac cgc ttc aag aac atg gtc atc gtc acc	869
Ala Leu Ile Lys Glu Asn His Arg Phe Lys Asn Met Val Ile Val Thr	
265 270 275	
act acc act gag tgc ctg agg cac ata cgg cag ttt ggt gcc ctg act	917
Thr Thr Thr Glu Cys Leu Arg His Ile Arg Gln Phe Gly Ala Leu Thr	
280 285 290	
gct gag gtg ggg gat atg aca gaa gac agc gcc cag gct ctc atc cga	965
Ala Glu Val Gly Asp Met Thr Glu Asp Ser Ala Gln Ala Leu Ile Arg	
295 300 305 310	
gaa gtg ctg atc aag gag ctt gct gaa ggc ttg ttg ctc caa att cag	1013
Glu Val Leu Ile Lys Glu Leu Ala Glu Gly Leu Leu Leu Gln Ile Gln	
315 320 325	
aaa tcc agg tgc ttg agg aat ctc atg aag acc cct ctc ttt gtg gtc	1061
Lys Ser Arg Cys Leu Arg Asn Leu Met Lys Thr Pro Leu Phe Val Val	
330 335 340	
atc act tgt gca atc cag atg ggt gaa agt gag ttc cac tct cac aca	1109
Ile Thr Cys Ala Ile Gln Met Gly Glu Ser Glu Phe His Ser His Thr	
345 350 355	
caa aca acg ctg ttc cat acc ttc tat gat ctg ttg ata cag aaa aac	1157
Gln Thr Thr Leu Phe His Thr Phe Tyr Asp Leu Leu Ile Gln Lys Asn	
360 365 370	
aaa cac aaa cat aaa ggt gtg gct gca agt gac ttc att cgg agc ctg	1205
Lys His Lys His Lys Gly Val Ala Ala Ser Asp Phe Ile Arg Ser Leu	
375 380 385 390	
gac cac tgt gga gac cta gct ctg gag ggt gtg ttc tcc cac aag ttt	1253
Asp His Cys Gly Asp Leu Ala Leu Glu Gly Val Phe Ser His Lys Phe	
395 400 405	
gat ttc gaa ctg cag gat gtg tcc agc gtg aat gag gat gtc ctg ctg	1301
Asp Phe Glu Leu Gln Asp Val Ser Ser Val Asn Glu Asp Val Leu Leu	
410 415 420	
aca act ggg ctc ctc tgt aaa tat aca gct caa agg ttc aag cca aag	1349
Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala Gln Arg Phe Lys Pro Lys	
425 430 435	

Fig. 1B

tat	aaa	ttc	ttt	cac	aag	tca	ttc	cag	gag	tac	aca	gca	gga	cga	aga	1397
Tyr	Lys	Phe	Phe	His	Lys	Ser	Phe	Gln	Glu	Tyr	Thr	Ala	Gly	Arg	Arg	
440						445					450					
ctc	agc	agt	tta	ttg	acg	tct	cat	gag	cca	gag	gag	gtg	acc	aag	ggg	1445
Leu	Ser	Ser	Leu	Leu	Thr	Ser	His	Glu	Pro	Glu	Glu	Val	Thr	Lys	Gly	
455					460					465					470	
aat	ggt	tac	ttg	cag	aaa	atg	gtt	tcc	att	tcg	gac	att	aca	tcc	act	1493
Asn	Gly	Tyr	Leu	Gln	Lys	Met	Val	Ser	Ile	Ser	Asp	Ile	Thr	Ser	Thr	
				475					480					485		
tat	agc	agc	ctg	ctc	cgg	tac	acc	tgt	ggg	tca	tct	gtg	gaa	gcc	acc	1541
Tyr	Ser	Ser	Leu	Leu	Arg	Tyr	Thr	Cys	Gly	Ser	Ser	Val	Glu	Ala	Thr	
			490					495					500			
agg	gct	gtt	atg	aag	cac	ctc	gca	gca	gtg	tat	caa	cac	ggc	tgc	ctt	1589
Arg	Ala	Val	Met	Lys	His	Leu	Ala	Ala	Val	Tyr	Gln	His	Gly	Cys	Leu	
			505				510					515				
ctc	gga	ctt	tcc	atc	gcc	aag	agg	cct	ctc	tgg	aga	cag	gaa	tct	ttg	1637
Leu	Gly	Leu	Ser	Ile	Ala	Lys	Arg	Pro	Leu	Trp	Arg	Gln	Glu	Ser	Leu	
	520					525					530					
caa	agt	gtg	aaa	aac	acc	act	gag	caa	gaa	att	ctg	aaa	gcc	ata	aac	1685
Gln	Ser	Val	Lys	Asn	Thr	Thr	Glu	Gln	Glu	Ile	Leu	Lys	Ala	Ile	Asn	
535					540					545					550	
atc	aat	tcc	ttt	gta	gag	tgt	ggc	atc	cat	tta	tat	caa	gag	agt	aca	1733
Ile	Asn	Ser	Phe	Val	Glu	Cys	Gly	Ile	His	Leu	Tyr	Gln	Glu	Ser	Thr	
				555					560					565		
tcc	aaa	tca	gcc	ctg	agc	caa	gaa	ttt	gaa	gct	ttc	ttt	caa	ggt	aaa	1781
Ser	Lys	Ser	Ala	Leu	Ser	Gln	Glu	Phe	Glu	Ala	Phe	Phe	Gln	Gly	Lys	
			570					575					580			
agc	tta	tat	atc	aac	tca	ggg	aac	atc	ccc	gat	tac	tta	ttt	gac	ttc	1829
Ser	Leu	Tyr	Ile	Asn	Ser	Gly	Asn	Ile	Pro	Asp	Tyr	Leu	Phe	Asp	Phe	
			585				590					595				
ttt	gaa	cat	ttg	ccc	aat	tgt	gca	agt	gct	ctg	gac	ttc	att	aaa	ctg	1877
Phe	Glu	His	Leu	Pro	Asn	Cys	Ala	Ser	Ala	Leu	Asp	Phe	Ile	Lys	Leu	
	600					605					610					
gac	ttt	tat	ggg	gga	gct	atg	gct	tca	tgg	gaa	aag	gct	gca	gaa	gac	1925
Asp	Phe	Tyr	Gly	Gly	Ala	Met	Ala	Ser	Trp	Glu	Lys	Ala	Ala	Glu	Asp	
615					620					625				630		
aca	ggt	gga	atc	cac	atg	gaa	gag	gcc	cca	gaa	acc	tac	att	ccc	agc	1973
Thr	Gly	Gly	Ile	His	Met	Glu	Glu	Ala	Pro	Glu	Thr	Tyr	Ile	Pro	Ser	
				635					640					645		
agg	gct	gta	tct	ttg	ttc	ttc	aac	tgg	aag	cag	gaa	ttc	agg	act	ctg	2021
Arg	Ala	Val	Ser	Leu	Phe	Phe	Asn	Trp	Lys	Gln	Glu	Phe	Arg	Thr	Leu	
			650					655					660			

Fig. 1C

gag gtc aca ctc cgg gat ttc agc aag ttg aat aag caa gat atc aca	2069
Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn Lys Gln Asp Ile Thr	
665 670 675	
tat ctg ggg aaa ata ttc agc tct gcc aca agc ctc agg ctg caa ata	2117
Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser Leu Arg Leu Gln Ile	
680 685 690	
aag aga tgt gct ggt gtg gct gga agc ctc agt ttg gtc ctc agc acc	2165
Lys Arg Cys Ala Gly Val Ala Gly Ser Leu Ser Leu Val Leu Ser Thr	
695 700 705 710	
tgt aag aac att tat tct ctc atg gtg gaa gcc agt ccc ctc acc ata	2213
Cys Lys Asn Ile Tyr Ser Leu Met Val Glu Ala Ser Pro Leu Thr Ile	
715 720 725	
gaa gat gag agg cac atc aca tct gta aca aac ctg aaa acc ttg agt	2261
Glu Asp Glu Arg His Ile Thr Ser Val Thr Asn Leu Lys Thr Leu Ser	
730 735 740	
att cat gac cta cag aat caa cgg ctg ccg ggt ggt ctg act gac agc	2309
Ile His Asp Leu Gln Asn Gln Arg Leu Pro Gly Gly Leu Thr Asp Ser	
745 750 755	
ttg ggt aac ttg aag aac ctt aca aag ctc ata atg gat aac ata aag	2357
Leu Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys	
760 765 770	
atg aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg aaa aac ctg	2405
Met Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu	
775 780 785 790	
aag aag atg tgt tta ttt cat ttg acc cac ttg tct gac att gga gag	2453
Lys Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu	
795 800 805	
gga atg gat tac ata gtc aag tct ctg tca agt gaa ccc tgt gac ctt	2501
Gly Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu	
810 815 820	
gaa gaa att caa tta gtc tcc tgc tgc ttg tct gca aat gca gtg aaa	2549
Glu Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys	
825 830 835	
atc cta gct cag aat ctt cac aat ttg gtc aaa ctg agc att ctt gat	2597
Ile Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp	
840 845 850	
tta tca gaa aat tac ctg gaa aaa gat gga aat gaa gct ctt cat gaa	2645
Leu Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu	
855 860 865 870	
ctg atc gac agg atg aac gtg cta gaa cag ctc acc gca ctg atg ctg	2693
Leu Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu	
875 880 885	

Fig. 1D

ccc tgg ggc tgt gac gtg caa ggc agc ctg agc agc ctg ttg aaa cat	2741
Pro Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His	
890 895 900	
ttg gag gag gtc cca caa ctc gtc aag ctt ggg ttg aaa aac tgg aga	2789
Leu Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg	
905 910 915	
ctc aca gat aca gag att aga att tta ggt gca ttt ttt gga aag aac	2837
Leu Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn	
920 925 930	
cct ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc	2885
Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser	
935 940 945 950	
agt gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aag caa	2933
Ser Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys Gln	
955 960 965	
tta gtg ttt ttt gac ttt agt act aaa gaa ttt cta cct gat cca gca	2981
Leu Val Phe Phe Asp Phe Ser Thr Lys Glu Phe Leu Pro Asp Pro Ala	
970 975 980	
tta gtc aga aaa ctt agc caa gtg tta tcc aag tta act ttt ctg caa	3029
Leu Val Arg Lys Leu Ser Gln Val Leu Ser Lys Leu Thr Phe Leu Gln	
985 990 995	
gaa gct agg ctt gtt ggg tgg caa ttt gat gat gat gat ctc agt gtt	3077
Glu Ala Arg Leu Val Gly Trp Gln Phe Asp Asp Asp Asp Leu Ser Val	
1000 1005 1010	
att aca ggt gct ttt aaa cta gta act gct taa ataaagtgtgta ctcgaagcca	3130
Ile Thr Gly Ala Phe Lys Leu Val Thr Ala *	
1015 1020	
gta	3133

Fig. 1E

1 ATGCTGAACGCTGGTCCCCTGGGCTCCCTTATTTCTTTCTCTATACTTTGTCTCTGTGTCTTTTTCTTTT
 TACGACTTGCGACCAGGGGACCCGAGGGAATAAAGAAAGAGATATGAAACAGAGACACAGAAAAAGAAAA
 1▷ M L N A G P L G S L I S F S I L C L C V F F F
 71 CCAAGTCTCTCGTTCCACCTAACGAGAAACACCCACAGAACAAGAAGGTATCTGGTCTACAAGAACTCGA
 GGTTCAGAGAGCAAGGTGGATTGCTCTTTGTGGGTGTCTTGTCTTCCATAGACCAGATGTTCTTGAGCT
 24▷ S K S L V P P N E K H P Q N K K V S G L Q E L E
 141 GGCCTCACTGAAACGGAAAGCAAATACAAAGAACTTTATTTTAAAAACATGTCTTGGTCTCCCAAGAAG
 CCGGAGTGACTTTGCCTTTTCGTTTATGTTTCTTTGAAATAAAATTTTGTACAGAACCAGAGGGTTCTTC
 47▷ A S L K R K A N T K K L Y F K N M S W S P K K
 211 AGGGCAATTGGATTGCTCAGCCAGAGACCCCTTGAGGCAGACACACAAGCGGCTGGACGTCGAGAGGAAC
 TCCCGTTAACCTAACGAGTCGGTCTCTGGGAACGTCCGTCTGTGTGTTCCCGACCTGCAGCTCTCCTTG
 71▷ R A I G L L S Q R P L Q A D T Q A A G R R E E
 281 ACATCGGCGGAAGAACATACAAGCAGCTGGACGTCCAGAGGACGTTGAAGGGAGAATGCTGGCGGAAGAG
 TGTAGCCGCCTTCTTGTATGTTTCGTTCGACCTGCAGGTCTCCTGCAACTTCCCTCTTACGACCGCCTTCTC
 94▷ H I G G R T Y K Q L D V Q R T L K G E C W R K S
 351 CACACAACAGACATCGGCACGCCAGCAGGCCATCCACCAGAGGAACGACTCGGAGTTTGGCCTGGAGGTG
 GTGTGTGTCTGTAGCCGTGCGGTCTCGGTAGGTGGTCTCCTTGCTGAGCCTCAAACCGGACCTCCAC
 117▷ T Q Q T S A R Q Q A I H Q R N D S E F G L E V
 421 AATTTTCATAAAGGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTTATAAAGCAAATCACAG
 TTAAAGTATTTCTGTTATCGGCTCGGGAATAAGTTTCTTACCCTTACTGACAATATTTTCGTTTGTGTCT
 141▷ N F I K D N S R A L I Q R M G M T V I K Q I T
 491 ATGACCTATTTGTATGGAATGTTCTGAATCGCGAAGAAGTAAACATCATTTTGTGCGAGAAGGTGGAGCA
 TACTGGATAAACATACCTTACAAGACTTAGCGCTTCTTCATTTGTAGTAAACGACGCTCTTCCACCTCGT
 164▷ D D L F V W N V L N R E E V N I I C C E K V E Q
 561 GGATGCTGCTAGAGGGATCATTCACATGATTTTGA AAAAGGGTTTCAGAGTCCTGTAACCTCTTTCTTAAA
 CCTACGACGATCTCCCTAGTAAGTGTACTAAAACTTTTTCCCAAGTCTCAGGACATTGGAGAAAGAATTT
 187▷ D A A R G I I H M I L K K G S E S C N L F L K
 631 TCCCTTAAGGAGTGGAACATCCTCTATTTTCAGGACTTGAATGGACAAAGTTTTGAGGAGACACAGAATT
 AGGGAATTCCCTCACCTTGATAGGAGATAAAGTCCCTGAACCTTACCTGTTTCAAACTCCTCTGTGTCTTAA
 211▷ S L K E W N Y P L F Q D L N G Q S F E E T Q N
 701 GGGTCTTCTTTAACATCACCTCTTCTCTAATAGGTCTTTTTCATCAGACATCAGAAGGAGACTTGGACGA
 CCCAGAAGAAATTGTAGTGGAGAAGAGATTATCCAGAAAAAGTAGTCTGTAGTCTTCCCTCTGAACCTGCT
 234▷ W V F F N I T S S L I G L F H Q T S E G D L D D
 771 TTTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACTTTTATCCCCTTGGTGAAGAT
 AAACCGAGTCCTAAATTTCTGAACATGGTATGGGGTAGAAAAGACTTGAAAATAGGGGAACCACTTCTA
 257▷ L A Q D L K D L Y H T P S F L N F Y P L G E D

Fig. 2A

841 ATTGACATTATTTTAACTTGAAAAGCACCTTCACAGAACCTGTCCTGTGGAGGAAGGACCAACACCATC
TAACTGTAATAAAAAATTGAACTTTTCGTGGAAGTGCTTTGGACAGGACACCTCCTTCCTGGTTGTGGTAG
281▷ I D I I F N L K S T F T E P V L W R K D Q H H

911 ACCGCGTGGAGCAGCTGACCCCTGAATGGCCTCCTGCAGGCTCTTCAGAGCCCCGTCATCATTGAAGGGGA
TGGCGCACCTCGTTCGACTGGGACTTACCGGAGGACGTCGAGAAAGTCTCGGGGACGTAGTAACCTCCCT
304▷ H R V E Q L T L N G L L Q A L Q S P C I I E G E

981 ATCTGGCAAAGGCAAGTCCACTCTGCTGCAGCGAATTGCCATGCTCTGGGGCTCCGGAAGTGCAAGGCT
TAGACCGTTTCCGTTTCAGGTGAGACGAGTTCGCTTAACGGTACGAGACCCCGAGGCCTTTCACGTTCCGA
327▷ S G K G K S T L L Q R I A M L W G S G K C K A

1051 CTGACCAAGTTCAAATTCGTCTTCTTCCTCCGTCTCAGCAGGGCCCAGGGTGGACTTTTTGAAACCCCTCT
GACTGGTTCAAGTTTAAGCAGAAGAAGGAGGCAGAGTCGTCCCGGTCCACCTGAAAACTTTGGGAGA
351▷ L T K F K F V F F L R L S R A Q G G L F E T L

1121 GTGATCAACTCCTGGATATACCTGGCACAATCAGGAAGCAGACATTTCATGGCCATGCTGCTGAAGCTGCG
CACTAGTTGAGGACCTATATGGACCGTGTTAGTCTTCGTCTGTAAGTACCGGTACGACGACTTCGACGC
374▷ C D Q L L D I P G T I R K Q T F M A M L L K L R

1191 GCAGAGGGTTCTTTTCTTCTTGATGGCTACAATGAATTCAAGCCCCAGAAGTGGCCAGAAATCGAAGCC
CGTCTCCCAAGAAAAGGAAGAACTACCGATGTTACTTAAAGTTCCGGGGTCTTGACGGGTCTTTAGCTTCGG
397▷ Q R V L F L L D G Y N E F K P Q N C P E I E A

1261 CTGATAAAGGAAAACCCGCTTCAAGAACATGGTTCATCGTCAACCACTACCACTGAGTGCCTGAGGCACA
GACTATTTTCTTTTGGTGGCGAAGTTCTTGTACCACTAGCAGTGGTGTGTTGACTCAGGACTCCGTGT
421▷ L I K E N H R F K N M V I V T T T T E C L R H

1331 TACGGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGGATATGACAGAAGACAGCGCCCAGGCTCTCATCCG
ATGCCGTCAAACCACGGGACTGACGACTCCACCCCTATACTGTCTTCTGTGCGGGTCCGAGAGTAGGC
444▷ I R Q F G A L T A E V G D M T E D S A Q A L I R

1401 AGAAGTGCTGATCAAGGAGCTTGCTGAAGGCTTGTGTCTCAAATTCAGAAATCCAGGTGCTTGAGGAAT
TCTTCACGACTAGTTCTTCGAACGACTTCCGAACAACGAGGTTTAAGTCTTTAGGTCCACGAACTCCTTA
467▷ E V L I K E L A E G L L L Q I Q K S R C L R N

1471 CTCATGAAGACCCCTCTCTTTGTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTC
GAGTACTTCTGGGGAGAGAAACACCACTAGTGAACACGTTAGGTCTACCCACTTTCACTCAAGGTGAGAG
491▷ L M K T P L F V V I T C A I Q M G E S E F H S

1541 ACACACAAACAACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACACAAACATAAAGG
TGTGTGTTTGTGTGCGACAAGGTATGGAAGATACTAGACAACCTATGTCTTTTTGTGTTGTGTTGTTATTTCC
514▷ H T Q T T L F H T F Y D L L I Q K N K H K H K G

1611 TGTGGCTGCAAGTGACTTCATTTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTGTTCTCC
ACACCGACGTTCACTGAAGTAAGCCTCGGACCTGGTGACACCTCTGGATCGAGACCTCCACACAAGAGG
537▷ V A A S D F I R S L D H C G D L A L E G V F S

1681 CACAAGTTTGATTTTGAAGTGCAGGATGTGTCCAGCGTGAATGAGGATGTCTGCTGACAACCTGGGCTCC
GTGTTCAAACATAAGCTTGACGTCTACACAGGTGCGACTTACTCTACAGGACGACTGTTGACCCGAGG
561▷ H K F D F E L Q D V S S V N E D V L L T T G L

Fig.2B

1751 TCTGTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAATTCTTTTACAAGTCATTCCAGGAGTACAC
 AGACATTTATATGTCGAGTTTCCAAGTTCCGTTTCATATTTAAGAAAGTGTTTCAGTAAGGTCCCTCATGTG
 584▷ L C K Y T A Q R F K P K Y K F F H K S F Q E Y T

1821 AGCAGGACGAAGACTCAGCAGTTTATTGACGTCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGGTTAC
 TCGTCTGCTTCTGAGTCGTCAAATAACTGCAGAGTACTCGGTCTCCTCCACTGGTTCCCTTACCAATG
 607▷ A G R R L S S L L T S H E P E E V T K G N G Y

1891 TTGCAGAAAATGGTTTCCATTTCCGACATTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGT
 AACGTCTTTTACCAAAGGTAAAGCCTGTAATGTAGGTGAATATCGTCGGACGAGGCCATGTGGACACCCA
 631▷ L Q K M V S I S D I T S T Y S S L L R Y T C G

1961 CATCTGTGGAAGCCACCAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGG
 GTAGACACCTTCGGTGGTCCCGACAATACTTCGTGGAGCGTCGTACATAGTTGTGCCGACGGAAGAGCC
 654▷ S S V E A T R A V M K H L A A V Y Q H G C L L G

2031 ACTTTCCATCGCCAAGAGGCCTCTCTGGAGACAGGAATCTTTGCAAAGTGTGAAAAACACCACTGAGCAA
 TGAAAGGTAGCGGTTCTCCGGAGAGACCTCTGTCCTTAGAAACGTTTCACACTTTTGTGGTGACTCGTT
 677▷ L S I A K R P L W R Q E S L Q S V K N T T E Q

2101 GAAATTCTGAAAGCCATAAACATCAATTCCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACAT
 CTTTAAGACTTTTCGGTATTTGTAGTTAAGGAAACATCTCACACCGTAGGTAAATATAGTTCTCTCATGTA
 701▷ E I L K A I N I N S F V E C G I H L Y Q E S T

2171 CCAAATCAGCCCTGAGCCAAGAATTTGAAGCTTTCTTTTCAAGGTAAAAGCTTATATATCAACTCAGGGAA
 GGTTTAGTCGGGACTCGGTTCTTAAACTTCGAAAGAAAGTTCCATTTTCGAATATATAGTTGAGTCCCTT
 724▷ S K S A L S Q E F E A F F Q G K S L Y I N S G N

2241 CATCCCCGATTACTTATTTGACTTCTTTGAACATTTGCCCAATTGTGCAAGTGCCCTGGACTTCATTAA
 GTAGGGGCTAATGAATAAACTGAAGAAACTTGTAACCGGTTAACACGTTACGGGACCTGAAGTAATTT
 747▷ I P D Y L F D F F E H L P N C A S A L D F I K

2311 CTGGACTTTTATGGGGGAGCTATGGCTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGAATCCACATGG
 GACCTGAAAATACCCCTCGATACCGAAGTACCCTTTTCCGACGTCTTCTGTGTCCACCTTAGGTGTACC
 771▷ L D F Y G G A M A S W E K A A E D T G G I H M

2381 AAGAGGCCCCAGAAACCTACATTCCCAGCAGGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAG
 TTCTCCGGGGTCTTTGGATGTAAGGGTCGTCCCGACATAGAAACAAGAAGTTGACCTTCGTCTTAAAGTC
 794▷ E E A P E T Y I P S R A V S L F F N W K Q E F R

2451 GACTCTGGAGGTCACACTCCGGGATTTTCAAGCAAGTTGAATAAGCAAGATATCAGATATCTGGGGAAAATA
 CTGAGACCTCCAGTGTGAGGCCCTAAAGTCGTTCAACTTATTCGTTCTATAGTCTATAGACCCCTTTTAT
 817▷ T L E V T L R D F S K L N K Q D I R Y L G K I

2521 TTCAGCTCTGCCACAAGCCTCAGGCTGCAAATAAAGAGATGTGCTGGTGTGGCTGGAAGCCTCAGTTTGG
 AAGTCGAGACGGTGTTCGGAGTCCGACGTTTATTTCTCTACACGACCACACCGACCTTCGGAGTCAAACC
 841▷ F S S A T S L R L Q I K R C A G V A G S L S L

2591 TCCTCAGCACCTGTAAGAACATTTATTCTCTCATGGTGAAGCCAGTCCCCTCACCATAGAAGATGAGAG
 AGGAGTCGTGGACATTCTTGTAATAAGAGAGTACCACCTTCGGTCAGGGGAGTGGTATCTTCTACTCTC
 864▷ V L S T C K N I Y S L M V E A S P L T I E D E R

2661 GCACATCACATCTGTAACAAACCTGAAAACCTTGAGTATTCATGACCTACAGAATCAACGGCTGCCGGGT
CGTGTAGTGTAGACATTGTTTGGACTTTTGGAACTCATAAGTACTGGATGTCTTAGTTGCCGACGGCCCA
887▷ H I T S V T N L K T L S I H D L Q N Q R L P G

2731 GGTCTGACTGACAGCTTGGGTAACCTGAAGAACCTTACAAAGCTCATAATGGATAACATAAAGATGAATG
CCAGACTGACTGTGCAACCCATTGAACTTCTTGGAAATGTTTCGAGTATTACCTATTGTATTTCTACTTAC
911▷ G L T D S L G N L K N L T K L I M D N I K M N

2801 AAGAAGATGCTATAAACTAGCTGAAGGCCTGAAAACCTGAAGAAGATGTGTTTATTTTCATTTGACCCA
TTCTTCTACGATATTTTGATCGACTTCCGGACTTTTGGACTTCTTCTACACAAATAAAGTAACTGGGT
934▷ E E D A I K L A E G L K N L K K M C L F H L T H

2871 CTTGTCTGACATTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGTGACCTTGAA
GAACAGACTGTAACCTCTCCCTTACCTAATGTATCAGTTCAGAGACAGTTCACTTGGGACACTGGAACCT
957▷ L S D I G E G M D Y I V K S L S S E P C D L E

2941 GAAATTC AATTAGTCTCCTGCTGCTTGTCTGCAAATGCAGTGAAAATCCTAGCTCAGAATCTTCACAATT
CTTTAAGTTAATCAGAGGACGACGAACAGACGTTTACGTCACTTTTAGGATCGAGTCTTAGAAGTGTTAA
981▷ E I Q L V S C C L S A N A V K I L A Q N L H N

3011 TGGTCAAACCTGAGCATTCTTGATTTATCAGAAAATTACCTGGAAAAAGATGGAAATGAAGCTCTTCATGA
ACCAGTTTGACTCGTAAGAACTAAATAGTCTTTTAATGGACCTTTTTCTACCTTTACTTTCGAGAACTACT
1004▷ L V K L S I L D L S E N Y L E K D G N E A L H E

3081 ACTGATCGACAGGATGAACGTGCTAGAACAGCTCACC GCACTGATGCTGCCCTGGGGCTGTGACGTGCAA
TGACTAGCTGTCTACTTGCACGATCTTGTGAGTGGCGTGACTACGACGGGACCCCGACACTGCACGTT
1027▷ L I D R M N V L E Q L T A L M L P W G C D V Q

3151 GGCAGCCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTCCCACTCGTCAAGCTTGGGTGAAAAACT
CCGTCCGACTCGTCCGACAACCTTGTAAACCTCCTCCAGGGTGTTGAGCAGTTTGAACCCCACTTTTGA
1051▷ G S L S S L L K H L E E V P Q L V K L G L K N

3221 GGAGACTCACAGATACAGAGATTAGAATTTTAGGTGCATTTTTTGGAAAGAACCCTCTGAAAAACTTCCA
CCTCTGAGTGTCTATGTCTCTAATCTTAAATCCACGTAAAAAACCTTTCTTGGGAGACTTTTGAAGGT
1074▷ W R L T D T E I R I L G A F F G K N P L K N F Q

3291 GCAGTTGAATTTGGCGGGAAATCGTGTGAGCAGTGTGATGGATGGCTTGCCTTCATGGGTGTATTTGAGAAT
CGTCAACTTAAACCGCCCTTTAGCACACTCGTCACTACCTACCGAACGGAAGTACCCACATAAACTCTTA
1097▷ Q L N L A G N R V S S D G W L A F M G V F E N

3361 CTTAAGCAATTAGTGTTTTTTGACTTTAGTACTAAAGAATTTCTACCTGATCCAGCATTAGTCAGAAAAC
GAATTCGTTAATCACAAAAAACTGAAATCATGATTTCTTAAAGATGGACTAGGTTCGTAATCAGTCTTTTG
1121▷ L K Q L V F F D F S T K E F L P D P A L V R K

3431 TTAGCCAAGTGTTATCCAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGTTGGGTGGCAATTTGATGATGA
AATCGGTTTCACAATAGGTTCAATTGAAAAGACGTTCTTCGATCCGAACAACCCACCGTTAAACTACTACT
1144▷ L S Q V L S K L T F L Q E A R L V G W Q F D D D

3501 TGATCTCAGTGTATTACAGATGAGAAAGCTCAGATGATTTGCCCATGGGTATATAAACTACTTCCTTAC
ACTAGAGTCACAATAATGTCTACTCTTTTCGAGTCTACTAAACGGGTACCCAATATTTTGATGAAGGAATG
1167▷ D L S V I T D E K A Q M I C P W V I K L L P Y

1191 T V A A S E L E F R S L A S

[illegible]

Fig. 2E

FFAR

CASP_3

ARA_5

MYSC_2a

LRR_P1_2

LRR_REC1_2

LRR

Cys

His

1 41 91 121 161 201 241 281 321 361 401 441 481 521 561 601 641 681 721 761 801 841 881 921 961 1001

Fig. 3

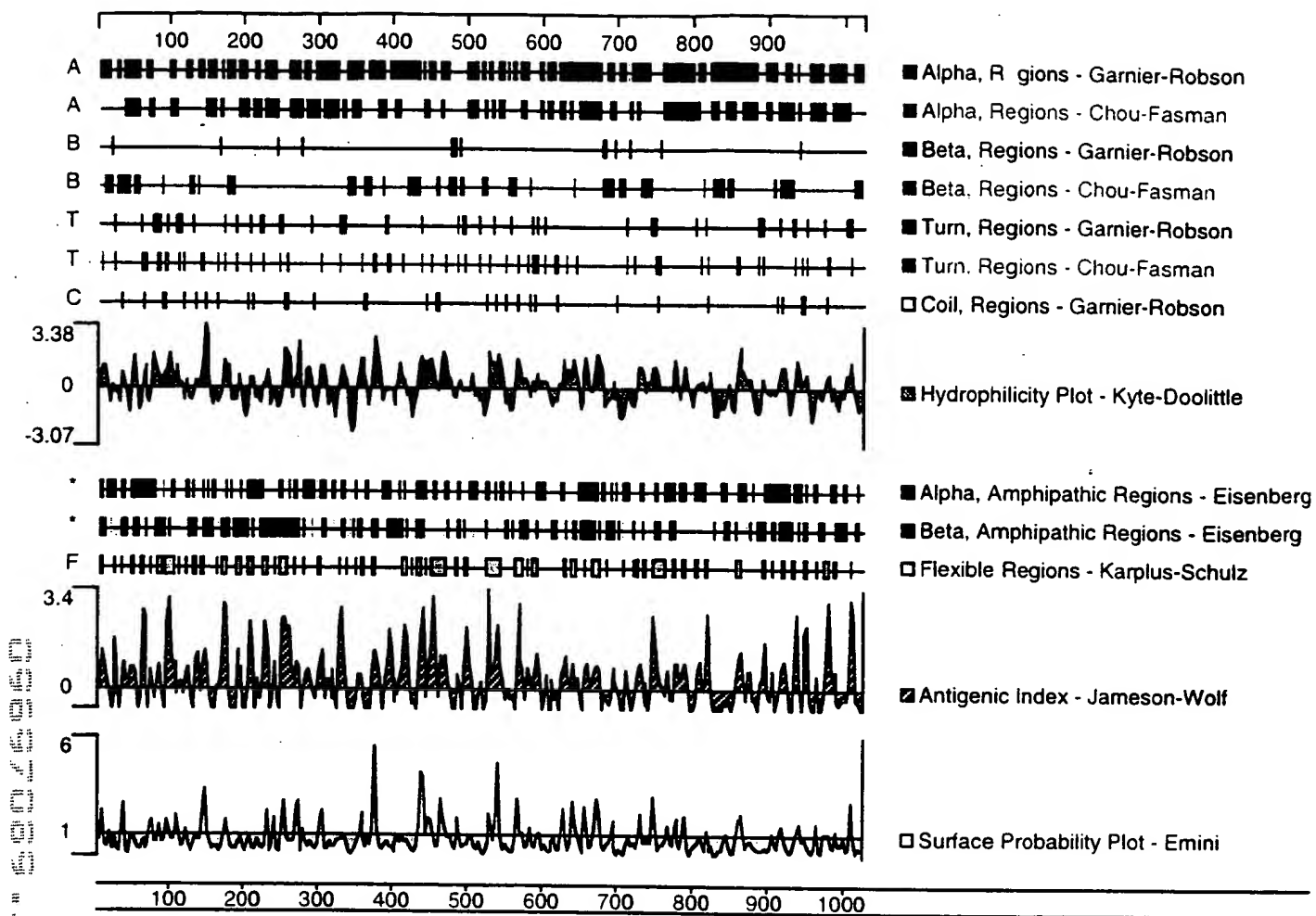


Fig.4

CARD: domain 1 of 1, from 2 to 88: score 16.0, E = 0.0065

SEQIDNO:7 *->aeddrlllrknrllellgeltlsglLdhLleknvLteeeeEkikaknt

+ + + + + d+L nvL++ee+ i +

CARD12 2 --NFIKDNSRALIQRMGMTVIKOITDDLFWNVNLNREEVNIICCEKV 46

```
trrdkareLiDsvqkkGnqAfgiFlgaLretdqelladlllde<*
```

```
++ dar i +++kkG++ ++F1 +L+e ++ l +dl +
```

CARD12 47 EQ-DAARGIIHMILKKGSESCNLFKSLKEWNYPLFODLNGOS 88

Fig. 5A

LRR: domain 1 of 4, from 764 to 791: score 0.6, E = 8.2e+02

```
SECTION:8      *->nLeeLdLsnN.Lt....slppgIfsnLp<*
```

nL++L ++n + +++ +l +q ++nL+

CARD12 764 NLTKLIMDNikMNeedaiKLAEG-LKNLK 791

Fig. 5B

LRR: domain 2 of 4, from 821 to 848: score 0.3, E = 9.3e+02

```
SEQID NO: 3      *->nLeeLdLsnN.Lt....slppqlfsnLp<*
```

Lee+ L ++ L+ + ++ ++nL

CARD12 821 DLEEIQLVSCcLSanavKILAONLHNLV 848

Fig. 5C

LRR: domain 3 of 4, from 849 to 872: score 11.2, E = 23

SEQ ID NO: 8 *->nLeeLdLsnN.LtslppgflfsnLp<-*

+L LdLs N L++ +++++ L

CARD12 849 KLSILDLSENyLEKDGNEALHELI 872

Fig. 5 D

LRR: domain 4 of 4, from 938 to 965: score 4.2, E = 2.5e+02

SEQ ID NO:8 *->nLeeLdLsnN.Lt.....slppgIfsnLp<*

$$n + L+L + N+ + + + + + + f+nL+$$

CARD12 938 NFOQLNLAGNrVSsdqwlAFMG-VFENLK 965

Fig. 5E

THE CHINESE

		E . L . L L . S E G E . G . G K . . L L . . I A . L W . S G	Consensus #1
		E Q L V L N G V L G A L N S V C I V E G E A G S G K S V L L Q K I A F L W G S G	Majority
		10 20 30 40	
1		E Q L T L N G L L Q A L Q S P C I I E G E S G K G K S T L L Q R I A M L W G S G	CARD12-C
1		E P L V L P E V F G N L N S V M C V E G E A G S G K T V L L K K I A F L W A S G	NAIP-C (SEQID NO:9)
		. C . . L . . F . . V F . L . L S . . R . . . G L C D Q L L . . . G . .	Consensus #1
		K C K A L T K F Q L V F F L S L S S T R A D G G L A S I L C D Q L L D I E G S V	Majority
		50 60 70 80	
41		K C K A L T K F K F V F F L R L S - - R A Q G G L F E T L C D Q L L D I P G T I	CARD12-C
41		C C P L L N R F Q L V F Y L S L S S T R P D E G L A S I I C D Q L L E K E G S V	NAIP-C
	 L . . . V L F L L D . Y . E C I . . L	Consensus #1
		T E Q T F R A I L L Q L K N Q V L F L L D G Y N E I K P Q N C S I P Q V I G A L	Majority
		90 100 110 120	
79		R K Q T F M A M L L K L R Q R V L F L L D G Y N E F K P Q N C P E - - - I E A L	CARD12-C
81		T E M C M R N I I Q Q L K N Q V L F L L D D Y K E I - - - - C S I P Q V I G K L	NAIP-C
		I . . N H T . . . R . I R E	Consensus #1
		I Q E N H L S K T C V L V A V T T E R A R D I R O F G A L I A E V G A F T E D S	Majority
		130 140 150 160	
116		I K E N H R F K N M V I V T T T T E C L R H I R Q F G A L T A E V G D M T E D S	CARD12-C
117		I Q K N H L S R T C L L I A V R T N R A R D I R R Y L E T I L E I Q A F P F Y N	NAIP-C
	 R K . . . L K T P L F V .	Consensus #1
		A V A L L R E V L I K E L A E L R G L L V Q I G K S Q S L Q N L Q K T P L F V A	Majority
		170 180 190 200	
156		A Q A L I R E V L I K E L A E - - G L L L Q I Q K S R C L R N L M K T P L F V V	CARD12-C
157		T V C I L R K L F S H N M T R L R K F M V Y F G K N Q S L Q K I Q K T P L F V A	NAIP-C
		. . C A F F L . . . N K	Consensus #1
		A I C A I Q W G E S E F D S S F T D V A V F K S F Y D L L I L K N K H K H K G V	Majority
		210 220 230 240	
194		I T C A I Q M G E S E F H S H - T Q T T L F H T F Y D L L I Q K N K H K H K G V	CARD12-C
197		A I C A - H W F Q Y P F D P S F D D V A V F K S Y M E R L S L R N K - - - - -	NAIP-C
		A C G . L A L . G . F S . . F . F . . . D V . E	Consensus #1
		A A A D I L K A T V S S C G D L A L E G V F S H K F D F E L D D V A E A G V D E	Majority
		250 260 270 280	
233		A A S D F I R S - L D H C G D L A L E G V F S H K F D F E L Q D V S - - S V N E	CARD12-C
230		A T A E I L K A T V S S C G E L A L K G F F S C C F E F N D D D L A E A G V D E	NAIP-C
		D . . L T . . L . . K . T A Q R . . P . Y . F F Q E . . A G . R L . . L	Consensus #1
		D V L L T T G L L S K F T A Q R L K P K Y K F L S K A F Q E F L A G R R L I S L	Majority
		290 300 310 320	
270		D V L L T T G L L C K Y T A Q R F K P K Y K F F H K S F Q E Y T A G R R L S S L	CARD12-C
270		D E D L T M C L M S K F T A Q R L R P F Y R F L S P A F O E F L A G M R L I E L	NAIP-C

Fig. 6A

	L . S E G L S S . Y L . Y																				Consensus #1	
	L T S D E Q E E V T L G L G H L Q Q I V S I S D I V S A Y S S L L N Y V S G L S																				Majority	
	330					340					350					360						
310	L	T	S	H	E	P	E	E	V	T	K	G	N	G	Y	L	Q	K	M	V	S	CARD12-C
310	L	D	S	D	R	Q	E	H	Q	D	L	G	L	Y	H	L	K	Q	I	N	S	NAIP-C
	370					380					390					400						
	S . . A H L L S L . . Q																				Consensus #1	
	S V E A G R A V V S H L A A V V D N K G S L L G L S I A D D Y L K H Q E S I S L																				Majority	
	370					380					390					400						
349	S	V	E	A	T	R	A	V	M	K	H	L	A	A	V	Y	Q	H	-	G	C	CARD12-C
350	S	T	K	A	G	P	K	I	V	S	H	L	L	H	L	V	D	N	K	E	S	NAIP-C
	410					420					430					440						
 L Q V Y Q . . T . .																				Consensus #1	
	Q M Q L L Q G V K N I T E Q A I L S A V S I N L L V L A G I T A Y Q S S T V A A																				Majority	
	410					420					430					440						
385	-	-	-	L	Q	S	V	K	N	T	T	E	Q	E	I	L	K	A	I	N	I	CARD12-C
390	Q	M	Q	L	R	G	L	W	Q	I	C	P	Q	A	Y	F	S	M	V	S	E	NAIP-C
	450					460					470					480						
 F . Q G . . L N Y . . . F F . H . P . . . S . L																				Consensus #1	
	A L S Q V L E A F L O G K S L T L G A G N L P D Y L F D F F D H L P E S A S A L																				Majority	
	450					460					470					480						
421	A	L	S	Q	E	F	E	A	F	F	Q	G	K	S	L	Y	I	N	S	G	N	CARD12-C
430	C	S	P	F	V	L	Q	-	F	L	O	G	R	T	L	T	L	G	A	L	N	NAIP-C
	490					500					510					520						
	. . I G P Y . .																				Consensus #1	
	D S I K L S I R G G A T A S R A K A A V L T G G I D K S E A P T I D E T Y I P A																				Majority	
	490					500					510					520						
461	D	F	I	K	L	D	F	Y	G	G	A	M	A	S	W	E	K	A	A	E	D	CARD12-C
464	R	S	I	H	F	S	I	R	G	N	K	T	S	P	R	A	H	F	S	V	L	NAIP-C
	530					540					550					560						
	. A W E L																				Consensus #1	
	S A V S L F N E W E Q E L A T L E V T V K S F S D L N K Q A I T D L G T G F S S																				Majority	
	530					540					550					560						
498	R	A	V	S	L	F	F	N	W	K	Q	E	F	R	T	L	E	V	T	L	R	CARD12-C
502	S	A	F	E	P	M	N	E	W	E	R	N	L	A	E	K	E	D	N	V	K	NAIP-C
	570					580					590					600						
 I . . C L . V																				Consensus #1	
	A S S L Q L Q I K R C A G V A G S L S L V L S T C K N I Y S L E V D A S D L T V																				Majority	
	570					580					590					600						
538	A	T	S	L	R	L	Q	I	K	R	C	A	G	V	A	G	S	L	S	L	V	CARD12-C
542	L	S	P	K	Q	Y	K	I	-	P	C	-	-	-	-	-	-	-	-	-	NAIP-C	
	610					620					630					640						
 S Q R L . . S																				Consensus #1	
	V G E D H L T I V T N L T V L S I H D L A S Q R L E G G L T D S L G N L K G L I																				Majority	
	610					620					630					640						
578	E	D	E	R	H	I	T	S	V	T	N	L	K	T	L	S	I	H	D	L	Q	CARD12-C
562	V	G	Q	D	M	L	E	I	L	-	-	M	T	V	F	S	-	-	-	-	A	NAIP-C

Fig. 6B

		. . I K C L S																				Consensus #1
		E L I R D A L E L S E A S A I K L A E G L K N L K K M C L I S L L E L S A A G E																				Majority
		650					660					670					680					
618	K L I	M D N I K M N E E D A I	K	L A E G L K N L K K M	C	L F H L T H L S	D I G E	CARD12-C														
592	E S I	R P A L E L S K A S V T	K	- - - - -	- - - - -	C S I S K L E L S	A A E Q	NAIP-C														
	 S L . S L E Q N																				Consensus #1
		G L L L I V K S L S S E P C D L E E I Q L V S C C L V A G A V O I L A Q I L H N																				Majority
		690					700					710					720					
658	G M D Y I V K S	L S S	S E P C D	L E E I Q L V S C C L S A N A V K I L A	Q N L H N	CARD12-C																
621	E L L L T L P S	L E S	- - - -	L E	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	V S G T I Q S Q D	Q I F P N	NAIP-C								
		L . K L . L . E G N I L .																				Consensus #1
		L V K L S I L D L S E L S V D L D G N I A V H S V I P D E F N V L E Q L T A L L																				Majority
		730					740					750					760					
698	L V K L S I L D L S	E N Y L E K D G N E A L H E L I	- D R M N V L E Q L T A L	L M	CARD12-C																	
648	L D K F - -	L C L K E L S V D L E G N I N V F S V I	P E E F P N F H H M E K L	L	NAIP-C																	
	 S . L L L . L D . E . .																				Consensus #1
		L Q I G A D V D G S L S S L V A S L E E V I S L V I L G L E G Q Q L T D T E I S																				Majority
		770					780					790					800					
737	L P W G C D V Q G S	L S S L L K H L E E V P Q L V K L G L K N W R L T D T E I R	CARD12-C																			
686	I Q I S A E Y D P - -	S K L V A S L P N F I S L K I L N L E G Q Q F P D E E T S	NAIP-C																			
	 A L . N L . L G K																				Consensus #1
		I L G A F I G L G S L S N L E E L I L A G G D V S S D G W L A F M G V F E V A K																				Majority
		810					820					830					840					
777	I L G A F F G K N P	L K N F Q Q L N L A G N R V S S D G W L A F M G V F E N L K	CARD12-C																			
724	E K F A Y I - L G S	L S N L E E L I L P T G D - - - - -	- - - - -	G I Y R V A K	NAIP-C																	
	 L L . L . F																				Consensus #1
		L L V F F D F S T K E F L P D P A L V Q Q L S Q V L S V L S F L Q T A R L V G W																				Majority
		850					860					870					880					
817	Q L V F F D F S T K E F L P D P A L V R K L S Q V L S K L T F L Q E A R L V G W	CARD12-C																				
753	L I I - - - - -	- - - - -	Q Q C Q Q L - H C L R V L S E F F K T - - - - -	NAIP-C																		
		. . . D D I																				Consensus #1
		Q L D D D S V V V I T G A F K L V T G																				Majority
		890																				
857	Q F D D D D L S V I T G A F K L V T A	CARD12-C																				
773	- L N D D S V V E I - - - - -	- - - - -	G	NAIP-C																		

Consensus 'Consensus #1': When all match the residue of CARD12-C show the residue of CARD12-C, otherwise show '.'.

Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #1' exactly.

Fig. 6C